Statistical Methods for Data Science

Mini Project #6

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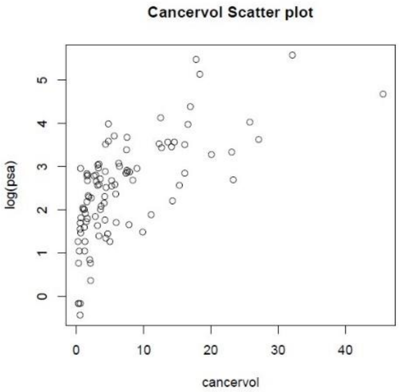
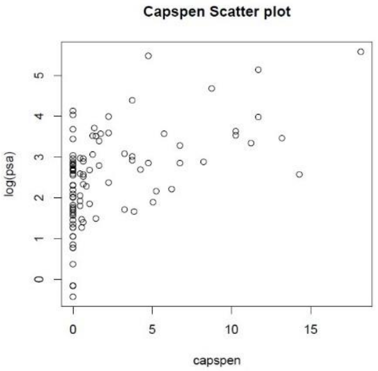
Problem 1:

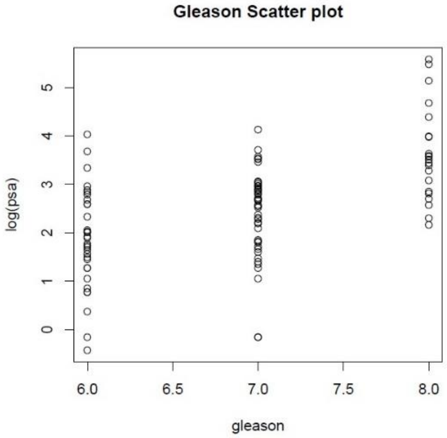
In order to build a linear model, we need to analyze the linear relationship between the predictors and the response variable (psa). To do this, we first plot each of the predictors against the response variable. Additionally, we apply a log transformation to the response variable, as this can improve the linear relationship.

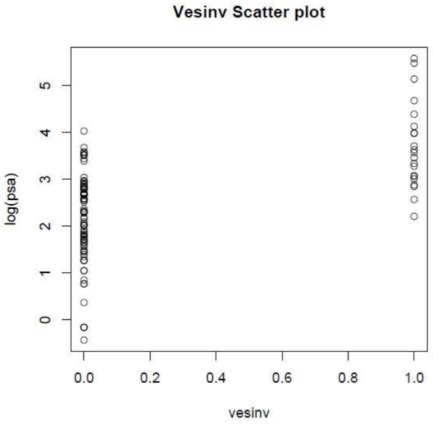
To gain a better understanding of the linear relationship between the variables, we calculate the correlation between each predictor and the response variable. If the correlation is positive, it indicates a positive linear relationship between the two variables. Conversely, if the correlation is negative, it suggests a negative linear relationship.

Upon observation, we found that there were four predictors (cancervol, vesinv, capspen, gleason) whose correlation with the response variable was above 0.5 and thus worth considering. Their scatterplots and correlations to further used to investigated their potential as predictors for the linear model.







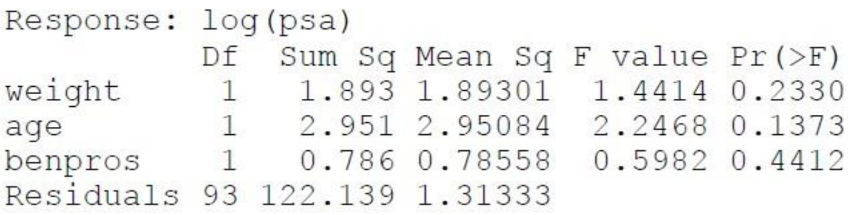


```
> cor(cancervol,log(psa))
[1] 0.6570739

> cor(vesinv,log(psa))

[1] 0.5663641
> cor(capspen,log(psa))
[1] 0.5180231
> cor(gleason,log(psa))
[1] 0.5390167
```

Vesinv is a categorical variable, while gleason is a numerical variable.

Despite the lack of a clear linear trend in the scatterplots, we relied on the correlation values to identify variables that could potentially affect the response variable.

To ensure that other variables do not have a significant impact on the response variable, we conducted a linear model analysis to observe their p-values. Specifically, we sought to test the null hypothesis that the slope values for weight, age, and benpros are zero, indicating that these variables do not have a significant impact on the response variable. Alternatively, we tested the alternative hypothesis that at least one of these variables has a non-zero slope value, indicating a significant impact on the response variable.

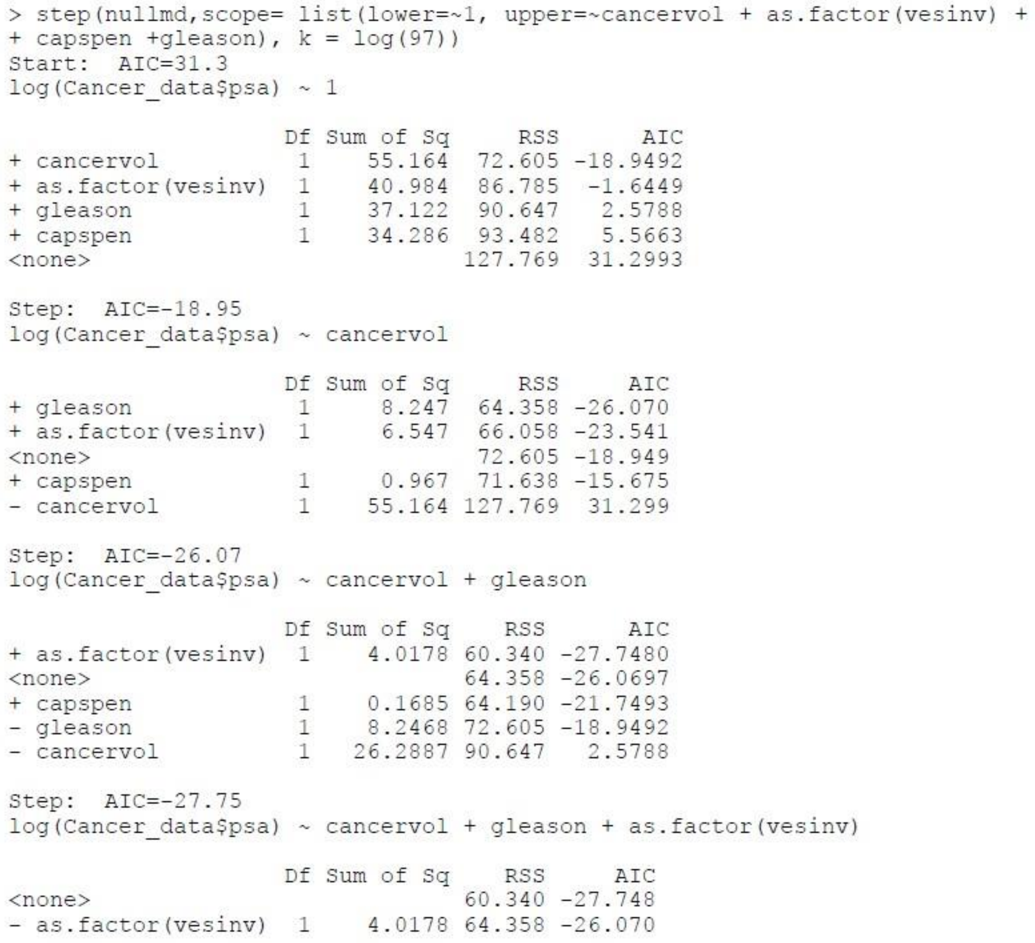


```
Response: log(psa)
          Df  Sum Sq Mean Sq F value Pr(>F)
weight     1   1.893 1.89301  1.4414 0.2330
age        1   2.951 2.95084  2.2468 0.1373
benpros    1   0.786 0.78558  0.5982 0.4412
Residuals 93 122.139 1.31333
```

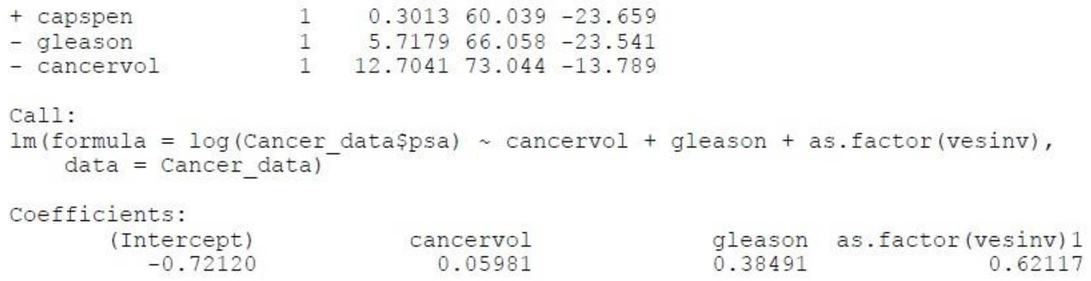
The linear model analysis revealed that all three variables (weight, age, and benpros) have a p-value greater than 0.05. This result suggests that we can accept the null hypothesis and reject the alternative hypothesis, allowing us to exclude these variables from our model.

The next step is to build the linear model using the remaining variables. To achieve this, we will utilize stepwise selection with Bayesian Information Criterion (BIC) to construct a model with a minimal number of variables while still maintaining a good fit.

Using stepwise selection with BIC is a more realistic approach, as it aims to build a model that effectively explains the variation in the response variable using only the most relevant predictors.



```
> step(nullmd,scope= list(lower=~1, upper=~cancervol + as.factor(vesinv) +
+ capspen +gleason), k = log(97))
Start:  AIC=31.3
log(Cancer_data$psa) ~ 1

                     Df Sum of Sq     RSS      AIC
+ cancervol           1    55.164  72.605 -18.9492
+ as.factor(vesinv)   1    40.984  86.785  -1.6449
+ gleason             1    37.122  90.647   2.5788
+ capspen             1    34.286  93.482   5.5663
<none>                            127.769  31.2993

Step:  AIC=-18.95
log(Cancer_data$psa) ~ cancervol

                     Df Sum of Sq     RSS     AIC
+ gleason             1     8.247  64.358 -26.070
+ as.factor(vesinv)   1     6.547  66.058 -23.541
<none>                             72.605 -18.949
+ capspen             1     0.967  71.638 -15.675
- cancervol           1    55.164 127.769  31.299

Step:  AIC=-26.07
log(Cancer_data$psa) ~ cancervol + gleason

                     Df Sum of Sq    RSS      AIC
+ as.factor(vesinv)   1    4.0178 60.340 -27.7480
<none>                            64.358 -26.0697
+ capspen             1    0.1685 64.190 -21.7493
- gleason             1    8.2468 72.605 -18.9492
- cancervol           1   26.2887 90.647   2.5788

Step:  AIC=-27.75
log(Cancer_data$psa) ~ cancervol + gleason + as.factor(vesinv)

                     Df Sum of Sq    RSS     AIC
<none>                            60.340 -27.748
- as.factor(vesinv)   1    4.0178 64.358 -26.070
```

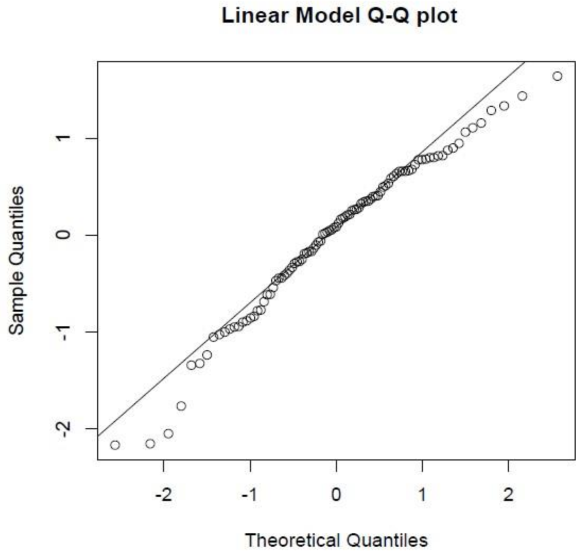


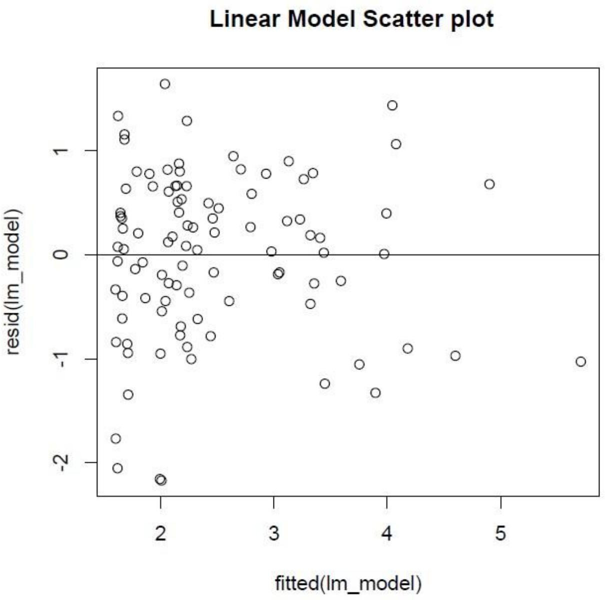
```
+ capspen             1    0.3013 60.039 -23.659
- gleason             1    5.7179 66.058 -23.541
- cancervol           1   12.7041 73.044 -13.789

Call:
lm(formula = log(Cancer_data$psa) ~ cancervol + gleason + as.factor(vesinv),
    data = Cancer_data)

Coefficients:
       (Intercept)           cancervol             gleason  as.factor(vesinv)1
          -0.72120             0.05981             0.38491             0.62117
```

The stepwise selection with BIC has suggested using three predictors, namely cancervol, gleason, and vesinv (a categorical variable).

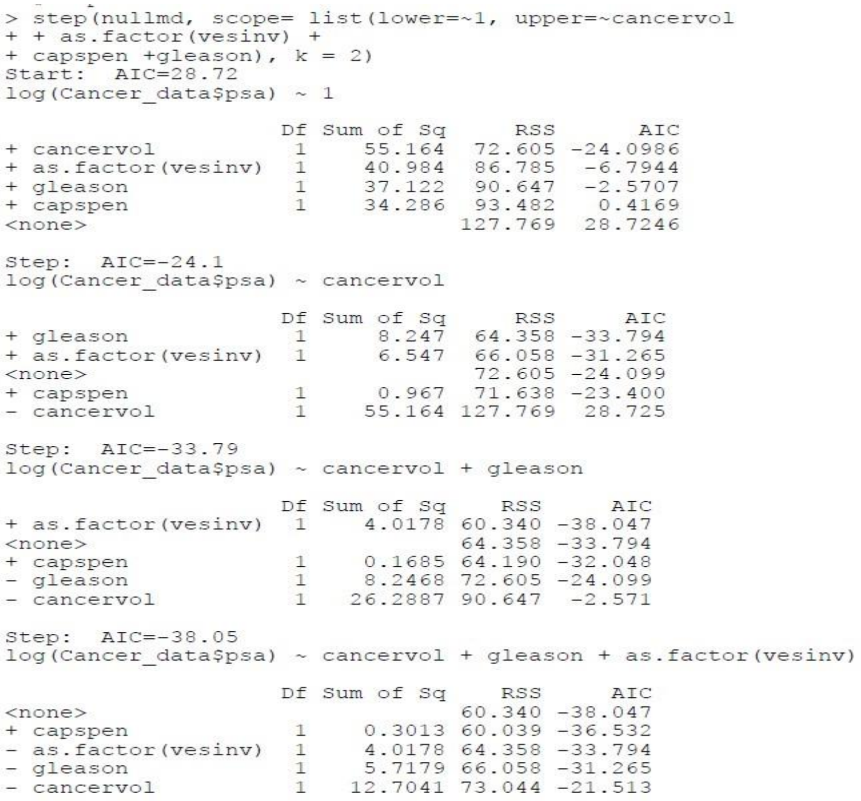
To verify the quality of the model, we will examine the fitted values and residuals. We will plot the fitted values against the residuals and also inspect the QQ plot for the residuals.

These plots will help us to assess the model's performance and check for any patterns or deviations from the assumptions of the linear regression model.

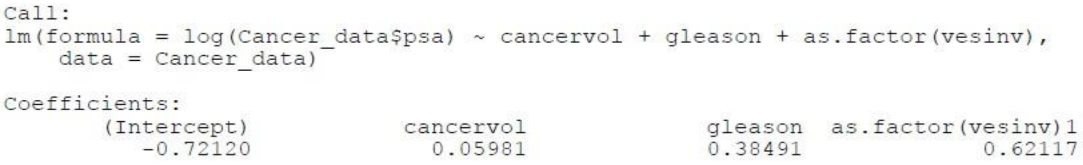




Stepwise model with AIC

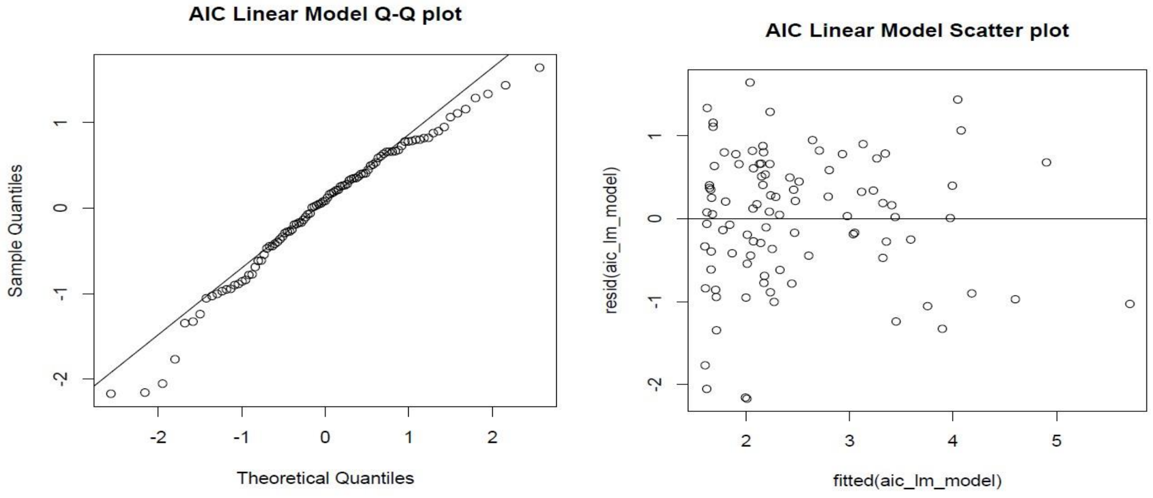


```
> step(nullmd, scope= list(lower=~1, upper=~cancervol
+ + as.factor(vesinv) +
+ capspen +gleason), k = 2)
Start:  AIC=28.72
log(Cancer_data$psa) ~ 1

                    Df Sum of Sq     RSS      AIC
+ cancervol          1    55.164  72.605 -24.0986
+ as.factor(vesinv)  1    40.984  86.785  -6.7944
+ gleason            1    37.122  90.647  -2.5707
+ capspen            1    34.286  93.482   0.4169
<none>                           127.769  28.7246

Step:  AIC=-24.1
log(Cancer_data$psa) ~ cancervol

                    Df Sum of Sq     RSS     AIC
+ gleason            1     8.247  64.358 -33.794
+ as.factor(vesinv)  1     6.547  66.058 -31.265
<none>                            72.605 -24.099
+ capspen            1     0.967  71.638 -23.400
- cancervol          1    55.164 127.769  28.725

Step:  AIC=-33.79
log(Cancer_data$psa) ~ cancervol + gleason

                    Df Sum of Sq    RSS     AIC
+ as.factor(vesinv)  1    4.0178 60.340 -38.047
<none>                           64.358 -33.794
+ capspen            1    0.1685 64.190 -32.048
- gleason            1    8.2468 72.605 -24.099
- cancervol          1   26.2887 90.647  -2.571

Step:  AIC=-38.05
log(Cancer_data$psa) ~ cancervol + gleason + as.factor(vesinv)

                    Df Sum of Sq    RSS     AIC
<none>                           60.340 -38.047
+ capspen            1    0.3013 60.039 -36.532
- as.factor(vesinv)  1    4.0178 64.358 -33.794
- gleason            1    5.7179 66.058 -31.265
- cancervol          1   12.7041 73.044 -21.513
```



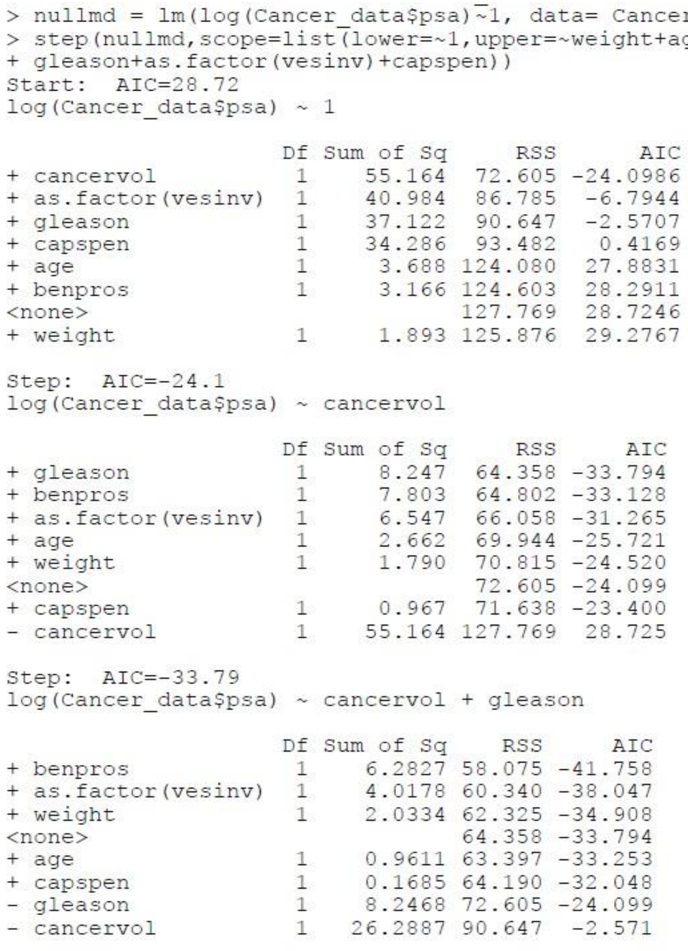
```
Call:
lm(formula = log(Cancer_data$psa) ~ cancervol + gleason + as.factor(vesinv),
    data = Cancer_data)

Coefficients:
      (Intercept)            cancervol              gleason  as.factor(vesinv)1
         -0.72120              0.05981              0.38491             0.62117
```

Scatter Plot and QQ plot for AIC

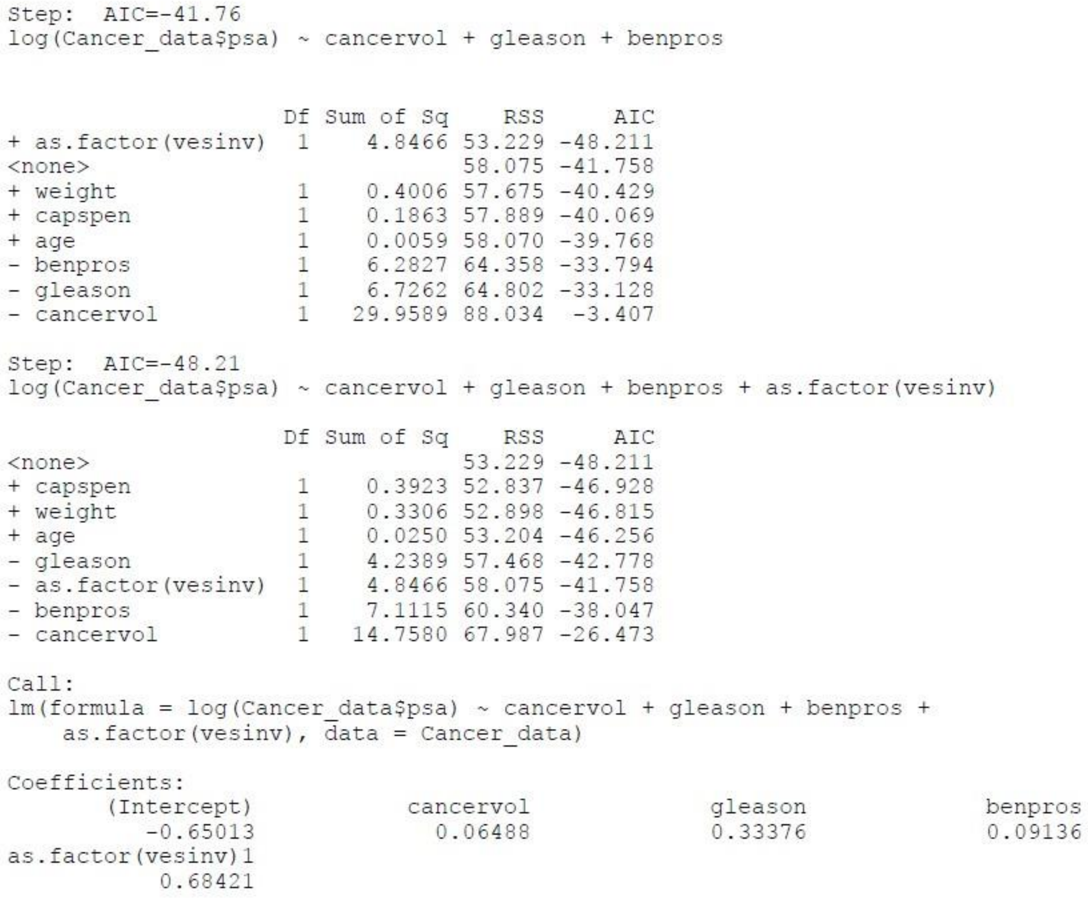


We can here observe that it is like Stepwise selection model calculated with BIC.

Although we initially excluded three variables, we want to create a stepwise selection using all variables to determine if there is a significant improvement in the model's outcome.

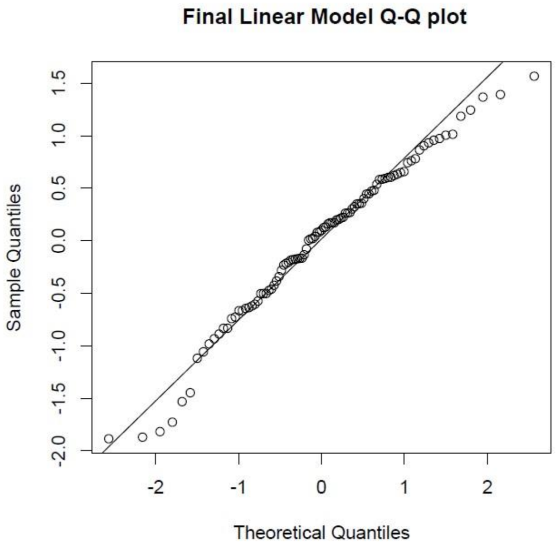


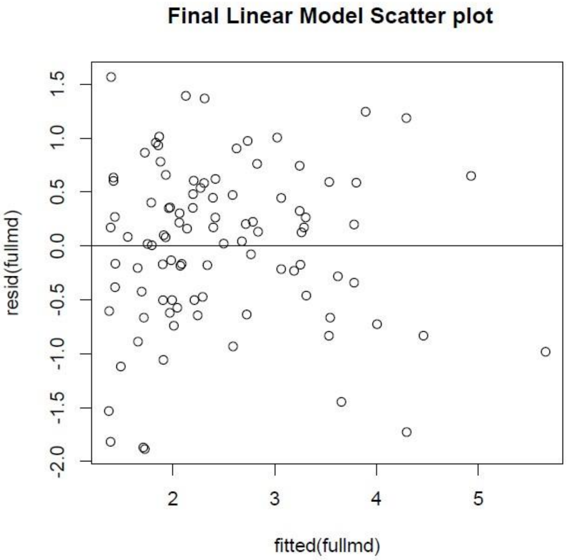
```
> nullmd = lm(log(Cancer_data$psa)~1, data= Cancer_data)
> step(nullmd,scope=list(lower=~1,upper=~weight+age+benpros+cancervol+
+ gleason+as.factor(vesinv)+capspen))
Start:  AIC=28.72
log(Cancer_data$psa) ~ 1

                     Df Sum of Sq     RSS      AIC
+ cancervol           1    55.164  72.605 -24.0986
+ as.factor(vesinv)   1    40.984  86.785  -6.7944
+ gleason             1    37.122  90.647  -2.5707
+ capspen             1    34.286  93.482   0.4169
+ age                 1     3.688 124.080  27.8831
+ benpros             1     3.166 124.603  28.2911
<none>                            127.769  28.7246
+ weight              1     1.893 125.876  29.2767

Step:  AIC=-24.1
log(Cancer_data$psa) ~ cancervol

                     Df Sum of Sq     RSS     AIC
+ gleason             1     8.247  64.358 -33.794
+ benpros             1     7.803  64.802 -33.128
+ as.factor(vesinv)   1     6.547  66.058 -31.265
+ age                 1     2.662  69.944 -25.721
+ weight              1     1.790  70.815 -24.520
<none>                             72.605 -24.099
+ capspen             1     0.967  71.638 -23.400
- cancervol           1    55.164 127.769  28.725

Step:  AIC=-33.79
log(Cancer_data$psa) ~ cancervol + gleason

                     Df Sum of Sq    RSS     AIC
+ benpros             1    6.2827 58.075 -41.758
+ as.factor(vesinv)   1    4.0178 60.340 -38.047
+ weight              1    2.0334 62.325 -34.908
<none>                           64.358 -33.794
+ age                 1    0.9611 63.397 -33.253
+ capspen             1    0.1685 64.190 -32.048
- gleason             1    8.2468 72.605 -24.099
- cancervol           1   26.2887 90.647  -2.571
```



```
Step:  AIC=-41.76
log(Cancer_data$psa) ~ cancervol + gleason + benpros


                     Df Sum of Sq    RSS     AIC
+ as.factor(vesinv)  1     4.8466 53.229 -48.211
<none>                            58.075 -41.758
+ weight             1     0.4006 57.675 -40.429
+ capspen            1     0.1863 57.889 -40.069
+ age                1     0.0059 58.070 -39.768
- benpros            1     6.2827 64.358 -33.794
- gleason            1     6.7262 64.802 -33.128
- cancervol          1    29.9589 88.034  -3.407

Step:  AIC=-48.21
log(Cancer_data$psa) ~ cancervol + gleason + benpros + as.factor(vesinv)

                     Df Sum of Sq    RSS     AIC
<none>                            53.229 -48.211
+ capspen            1     0.3923 52.837 -46.928
+ weight             1     0.3306 52.898 -46.815
+ age                1     0.0250 53.204 -46.256
- gleason            1     4.2389 57.468 -42.778
- as.factor(vesinv)  1     4.8466 58.075 -41.758
- benpros            1     7.1115 60.340 -38.047
- cancervol          1    14.7580 67.987 -26.473

Call:
lm(formula = log(Cancer_data$psa) ~ cancervol + gleason + benpros + 
    as.factor(vesinv), data = Cancer_data)

Coefficients:
      (Intercept)          cancervol            gleason            benpros  
         -0.65013            0.06488            0.33376            0.09136  
as.factor(vesinv)1  
          0.68421  
```

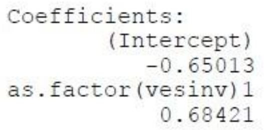
It can be noted that the model does not incorporate the three variables that were initially excluded, while all the other variables are present. To evaluate whether this model is an improvement, we examine the scatter plots of fitted versus residual values and the QQ plot for the residuals.





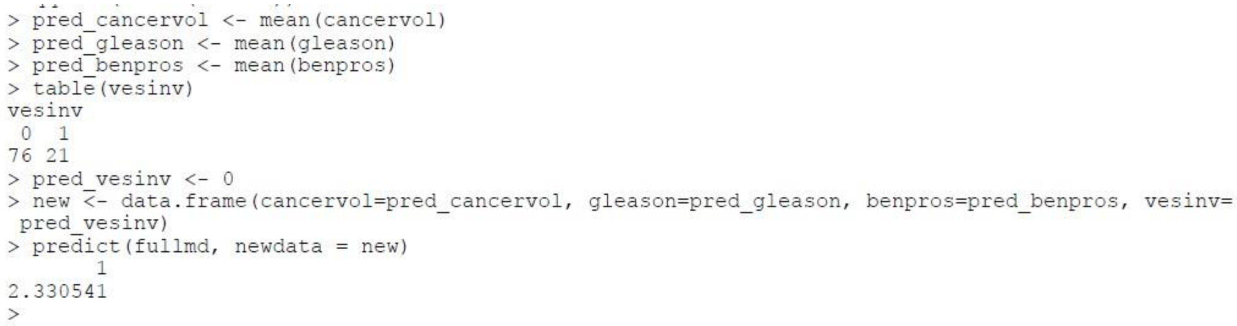
The QQ plot clearly indicates that the residuals conform better to a normal distribution, thus affirming the inclusion of these four predictors (cancervol, gleason, benpros, vesinv) in the final model.

The Regression Result:



```
Coefficients:
       (Intercept)            cancervol            gleason             benpros
          -0.65013              0.06488            0.33376             0.09136
as.factor(vesinv)1
           0.68421
```

Predicted PSA:



```
> pred_cancervol <- mean(cancervol)
> pred_gleason <- mean(gleason)
> pred_benpros <- mean(benpros)
> table(vesinv)
vesinv
 0  1
76 21
> pred_vesinv <- 0
> new <- data.frame(cancervol=pred_cancervol, gleason=pred_gleason, benpros=pred_benpros, vesinv=
 pred_vesinv)
> predict(fullmd, newdata = new)
       1
2.330541
>
```

Formula:

-0.65013+ (0.06488*pred_cancervol) +(0.33376*pred_gleason) +(0.09136*pred_benpros) +(0.68421*pred_vesinv)

Predicted_PSA = 2.330541

Rcode:

```
> Cancer_data=read.csv("C:/Users/yxa210024/Desktop/Masters/spring2023/Stats
for DS/mini_project6/
prostate_cancer.csv")
> attach(Cancer_data)
> plot(cancervol,log(psa), main = "Cancervol Scatter plot")
> cor(cancervol,log(psa))
[1] 0.6570739
> plot(benpros,log(psa), main = " Benpros Scatter plot ")
> cor(benpros,log(psa))
[1] 0.1574016
> plot(vesinv,log(psa), main = " Vesinv Scatter plot ")
> cor(vesinv,log(psa))
[1] 0.5663641
> plot(capspen,log(psa), main = " Capspen Scatter plot ")
> cor(capspen,log(psa))
[1] 0.5180231
> plot(gleason,log(psa), main = " Gleason Scatter plot ")
> cor(gleason,log(psa))
[1] 0.5390167
```

```
> #we could not show a linear trend with psa-response variable from any above
variables
> cor(cancervol,psa)
[1] 0.6241506
> # Cancervol and psa have a strong positive correlation
> table(Cancer_data$vesinv)
0 1
76 21
> table(Cancer_data$gleason)
6 7 8
33 43 21
> # individual variables
> Ind_varia_1 <- lm(log(psa)~weight+age+benpros)
> summary(Ind_varia_1)
Call:
lm(formula = log(psa) ~ weight + age + benpros)
Residuals:
Min 1Q Median 3Q Max
-2.6950 -0.7076 -0.0243 0.6254 3.0399
Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept) 1.065917 1.051430 1.014 0.313
weight 0.001837 0.002707 0.679 0.499
age 0.019484 0.016907 1.152 0.252
benpros 0.033462 0.043265 0.773 0.441
Residual standard error: 1.146 on 93 degrees of freedom
Multiple R-squared: 0.04406, Adjusted R-squared: 0.01322
F-statistic: 1.429 on 3 and 93 DF, p-value: 0.2394
> anova(Ind_varia_1)
Analysis of Variance Table
Response: log(psa)
Df Sum Sq Mean Sq F value Pr(>F)
weight 1 1.893 1.89301 1.4414 0.2330
age 1 2.951 2.95084 2.2468 0.1373
benpros 1 0.786 0.78558 0.5982 0.4412
Residuals 93 122.139 1.31333
> step(nullmd,scope= list(lower=~1, upper=~cancervol + as.factor(vesinv) +
+ capspen +gleason), k = log(97))
Start: AIC=31.3
log(Cancer_data$psa) ~ 1
Df Sum of Sq RSS AIC
+ cancervol 1 55.164 72.605 -18.9492
+ as.factor(vesinv) 1 40.984 86.785 -1.6449
+ gleason 1 37.122 90.647 2.5788
+ capspen 1 34.286 93.482 5.5663
<none> 127.769 31.2993
Step: AIC=-18.95
log(Cancer_data$psa) ~ cancervol
Df Sum of Sq RSS AIC
+ gleason 1 8.247 64.358 -26.070
+ as.factor(vesinv) 1 6.547 66.058 -23.541
<none> 72.605 -18.949
+ capspen 1 0.967 71.638 -15.675
- cancervol 1 55.164 127.769 31.299
Step: AIC=-26.07
log(Cancer_data$psa) ~ cancervol + gleason
Df Sum of Sq RSS AIC
```

```
+ as.factor(vesinv) 1 4.0178 60.340 -27.7480
<none> 64.358 -26.0697
+ capspen 1 0.1685 64.190 -21.7493
- gleason 1 8.2468 72.605 -18.9492
- cancervol 1 26.2887 90.647 2.5788
Step: AIC=-27.75
log(Cancer_data$psa) ~ cancervol + gleason + as.factor(vesinv)
Df Sum of Sq RSS AIC
<none> 60.340 -27.748
- as.factor(vesinv) 1 4.0178 64.358 -26.070
+ capspen 1 0.3013 60.039 -23.659
- gleason 1 5.7179 66.058 -23.541
- cancervol 1 12.7041 73.044 -13.789
Call:
lm(formula = log(Cancer_data$psa) ~ cancervol + gleason + as.factor(vesinv),
data = Cancer_data)
Coefficients:
(Intercept) cancervol gleason as.factor(vesinv)1
-0.72120 0.05981 0.38491 0.62117
> lm_model <- lm(formula = log(Cancer_data$psa) ~ cancervol + gleason +
as.factor(vesinv),
+ data = Cancer_data)
> fitted(lm_model)
1 2 3 4 5 6 7 8
1.621772 1.995423 2.009114 1.606299 1.714907 1.609211 1.713645 1.707532
9 10 11 12 13 14 15 16
2.000615 1.662816 1.665083 1.603786 2.272428 2.235948 2.173779 1.867286
17 18 19 20 21 22 23 24
2.012494 2.178928 1.622448 2.044805 1.777184 2.442488 1.623136 2.327881
25 26 27 28 29 30 31 32
1.676626 1.843271 2.072803 2.013289 2.142419 2.254239 1.668217 1.659891
33 34 35 36 37 38 39 40
1.803406 1.648700 1.647498 2.194875 2.605562 2.067946 3.449465 2.106310
41 42 43 44 45 46 47 48
2.469297 2.225649 1.695109 2.324352 2.238592 2.287770 3.896381 2.163994
49 50 51 52 53 54 55 56
1.932482 1.790881 2.151098 1.902856 2.072803 2.476516 3.753908 2.186184
57 58 59 60 61 62 63 64
2.130977 1.683032 2.460750 2.145841 1.683032 3.036327 3.322233 3.049784
65 66 67 68 69 70 71 72
2.062287 2.230751 2.424084 2.513007 1.626420 2.169808 2.978583 2.163994
73 74 75 76 77 78 79 80
2.794946 3.355889 4.180648 3.591359 2.804512 3.116519 3.440954 3.322233
81 82 83 84 85 86 87 88
2.233335 2.709187 3.407764 3.230486 2.642748 4.600958 2.039170 2.931750
89 90 91 92 93 94 95 96
3.972762 3.263915 3.130873 3.345224 3.992835 5.706992 4.077249 4.044801
97
4.901464
> resid(lm_model)
1 2 3 4 5 6
-2.051017742 -2.155592069 -2.169283217 -1.766467289 -1.344723308 -0.839103198
7 8 9 10 11 12
-0.943536330 -0.857380755 -0.950492987 -0.612693563 -0.395041143 -0.333744995
13 14 15 16 17 18
-1.002386909 -0.886058813 -0.773828390 -0.417312530 -0.542547954 -0.688949779
19 20 21 22 23 24
```

```
-0.062410428 -0.444811303 -0.137216562 -0.782547145 0.076873774 -0.617873784
25 26 27 28 29 30
0.053434939 -0.073245855 -0.272744852 -0.193266463 -0.292390854 -0.364294235
31 32 33 34 35 36
0.251789351 0.350066681 0.206551871 0.371257071 0.402515144 -0.104864556
37 38 39 40 41 42
-0.445578216 0.122029823 -1.239434362 0.173722439 -0.169315133 0.084309118
43 44 45 46 47 48
0.634897121 0.045611531 0.281440234 0.262221602 -1.326367935 0.406019732
49 50 51 52 53 54
0.657535525 0.799136326 0.508881711 0.777137269 0.607190479 0.213506462
55 56 57 58 59 60
-1.053890080 0.533794522 0.659021739 1.106966418 0.349255331 0.664164401
61 62 63 64 65 66
1.156981333 -0.186313946 -0.472220598 -0.169799778 0.817697337 0.659232033
67 68 69 70 71 72
0.495900852 0.446994143 1.333581904 0.800196617 0.031396990 0.875994660
73 74 75 76 77 78
0.265074697 -0.275907564 -0.900639088 -0.251363139 0.585489964 0.323482255
79 80 81 82 83 84
R Console Page 5
0.019046625 0.187758777 1.286652644 0.820813657 0.162247460 0.339525077
85 86 87 88 89 90
0.947249952 -0.970953240 1.640820376 0.778254854 0.007237055 0.726087105
91 92 93 94 95 96
0.899128837 0.784777498 0.397159326 -1.026992978 1.062752087 1.435200389
97
0.678537942
> plot(fitted(lm_model),resid(lm_model), main = " Linear Model Scatter plot")
> abline(h=0)
> qqnorm(resid(lm_model), main = " Linear Model Q-Q plot")
> qqline(resid(lm_model))
> #Stepwise Selection with AIC
> step(nullmd, scope= list(lower=~1, upper=~cancervol
+ + as.factor(vesinv) +
+ capspen +gleason), k = 2)
Start: AIC=28.72
log(Cancer_data$psa) ~ 1
Df Sum of Sq RSS AIC
+ cancervol 1 55.164 72.605 -24.0986
+ as.factor(vesinv) 1 40.984 86.785 -6.7944
+ gleason 1 37.122 90.647 -2.5707
+ capspen 1 34.286 93.482 0.4169
<none> 127.769 28.7246
Step: AIC=-24.1
log(Cancer_data$psa) ~ cancervol
Df Sum of Sq RSS AIC
+ gleason 1 8.247 64.358 -33.794
+ as.factor(vesinv) 1 6.547 66.058 -31.265
<none> 72.605 -24.099
+ capspen 1 0.967 71.638 -23.400
- cancervol 1 55.164 127.769 28.725
Step: AIC=-33.79
log(Cancer_data$psa) ~ cancervol + gleason
Df Sum of Sq RSS AIC
+ as.factor(vesinv) 1 4.0178 60.340 -38.047
<none> 64.358 -33.794
```

```
+ capspen 1 0.1685 64.190 -32.048
- gleason 1 8.2468 72.605 -24.099
- cancervol 1 26.2887 90.647 -2.571
Step: AIC=-38.05
log(Cancer_data$psa) ~ cancervol + gleason + as.factor(vesinv)
Df Sum of Sq RSS AIC
<none> 60.340 -38.047
+ capspen 1 0.3013 60.039 -36.532
- as.factor(vesinv) 1 4.0178 64.358 -33.794
- gleason 1 5.7179 66.058 -31.265
- cancervol 1 12.7041 73.044 -21.513
Call:
lm(formula = log(Cancer_data$psa) ~ cancervol + gleason + as.factor(vesinv),
data = Cancer_data)
Coefficients:
(Intercept) cancervol gleason as.factor(vesinv)1
-0.72120 0.05981 0.38491 0.62117
> aic_lm_model <- lm(formula = log(Cancer_data$psa) ~ cancervol + gleason +
+ as.factor(vesinv),
+ data = Cancer_data)
> plot(fitted(aic_lm_model),resid(aic_lm_model), main = "AIC Linear Model
Scatter plot")
> abline(h=0)
> qqnorm(resid(aic_lm_model) , main = "AIC Linear Model Q-Q plot")
> qqline(resid(aic_lm_model))

> nullmd = lm(log(Cancer_data$psa)~1, data= Cancer_data)
> step(nullmd,scope=list(lower=~1,upper=~weight+age+benpros+cancervol+
+ gleason+as.factor(vesinv)+capspen))
Start: AIC=28.72
log(Cancer_data$psa) ~ 1
Df Sum of Sq RSS AIC
+ cancervol 1 55.164 72.605 -24.0986
+ as.factor(vesinv) 1 40.984 86.785 -6.7944
+ gleason 1 37.122 90.647 -2.5707
+ capspen 1 34.286 93.482 0.4169
+ age 1 3.688 124.080 27.8831
+ benpros 1 3.166 124.603 28.2911
<none> 127.769 28.7246
+ weight 1 1.893 125.876 29.2767
Step: AIC=-24.1
log(Cancer_data$psa) ~ cancervol
Df Sum of Sq RSS AIC
+ gleason 1 8.247 64.358 -33.794
+ benpros 1 7.803 64.802 -33.128
+ as.factor(vesinv) 1 6.547 66.058 -31.265
+ age 1 2.662 69.944 -25.721
+ weight 1 1.790 70.815 -24.520
<none> 72.605 -24.099
+ capspen 1 0.967 71.638 -23.400
- cancervol 1 55.164 127.769 28.725
Step: AIC=-33.79
log(Cancer_data$psa) ~ cancervol + gleason
Df Sum of Sq RSS AIC
+ benpros 1 6.2827 58.075 -41.758
+ as.factor(vesinv) 1 4.0178 60.340 -38.047
+ weight 1 2.0334 62.325 -34.908
```

```
<none> 64.358 -33.794
+ age 1 0.9611 63.397 -33.253
+ capspen 1 0.1685 64.190 -32.048
- gleason 1 8.2468 72.605 -24.099
- cancervol 1 26.2887 90.647 -2.571
Step: AIC=-41.76
log(Cancer_data$psa) ~ cancervol + gleason + benpros
Df Sum of Sq RSS AIC
+ as.factor(vesinv) 1 4.8466 53.229 -48.211
<none> 58.075 -41.758
+ weight 1 0.4006 57.675 -40.429
+ capspen 1 0.1863 57.889 -40.069
+ age 1 0.0059 58.070 -39.768
- benpros 1 6.2827 64.358 -33.794
- gleason 1 6.7262 64.802 -33.128
- cancervol 1 29.9589 88.034 -3.407
Step: AIC=-48.21
log(Cancer_data$psa) ~ cancervol + gleason + benpros + as.factor(vesinv)
Df Sum of Sq RSS AIC
<none> 53.229 -48.211
+ capspen 1 0.3923 52.837 -46.928
+ weight 1 0.3306 52.898 -46.815
+ age 1 0.0250 53.204 -46.256
- gleason 1 4.2389 57.468 -42.778
- as.factor(vesinv) 1 4.8466 58.075 -41.758
- benpros 1 7.1115 60.340 -38.047
- cancervol 1 14.7580 67.987 -26.473
Call:
lm(formula = log(Cancer_data$psa) ~ cancervol + gleason + benpros +
as.factor(vesinv), data = Cancer_data)
Coefficients:
(Intercept) cancervol gleason benpros
-0.65013 0.06488 0.33376 0.09136
as.factor(vesinv)1
0.68421
> fullmd <- lm(formula = log(Cancer_data$psa) ~ cancervol + gleason + benpros
+
+ as.factor(vesinv), data = Cancer_data)
> plot(fitted(fullmd),resid(fullmd) , main = " Final Linear Model Scatter
plot")
> abline(h=0)
> qqnorm(resid(fullmd) , main = " Final Linear Model Q-Q plot")
> qqline(resid(fullmd))
> pred_cancervol <- mean(cancervol)
> pred_gleason <- mean(gleason)
> pred_benpros <- mean(benpros)
> table(vesinv)
vesinv
0 1
76 21
> pred_vesinv <- 0
> new <- data.frame(cancervol=pred_cancervol, gleason=pred_gleason,
benpros=pred_benpros, vesinv=
pred_vesinv)
> predict(fullmd, newdata = new)
1
2.330541
```